QM protein - protein search, using sw model

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Run on: September 24, 2004, 13:44:25 ; Search time 125 seconds
                 (without alignments)
                 560.574 Million cell updates/sec

Title: US-09-554-465-75
Perfect score: 1324
Sequence: 1 EVQLLEQSGAELVRPGTSVK..........CQNDYSYPLTFGAGTKLEIK 248
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :   1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2002as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 A_Geneseq_29Jan04:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1324	100.0	248	2	AAY17964	Mouse scFv
2	1261	95.2	248	2	AAY17960	Mouse scF
3	1203	90.9	248	2	AAY17965	Mouse scF
4	1177	88.9	258	5	AAU72865	P5-2 sing
5	1060	80.1	242	2	AAY17959	Mouse scF
6	1057	79.8	242	2	AAY17957	Mouse scF
7	1054	79.6	242	2	AAY17961	Mouse scF
8	1027	77.6	258	5	AAU72871	Mouse scF
9	1027	77.6	258	5	AAU72875	3B10xP4-3
10	1022	77.2	288	2	AAW82743	Human NKG
11	1022	77.2	673	2	AAW82742	Plasmid p
12	1009	76.2	242	4	AAB31422	Protein u
13	1004.5	75.9	262	4	AAB31421	Protein u
14	995.5	75.2	242	4	ADD13792	Plasmid p
15	990.5	74.8	500	7	AAU72870	P5-23 sin
16	988.5	74.7	255	5	AAU72870	Protein u
17	988	74.6	272	4	AAB31423	Protein u
18	978.5	73.9	259	5	AAU72862	P4-3 sing
19	978	73.9	444	6	ABJ39018	Protein u
20	972	73.4	532	2	AAW35565	HindIII-E
21	956	72.2	580	2	AAW90217	Bispecifi
22	953	72.0	556	2	AAW90218	Bispecifi
23	940.5	71.0	251	2	AAY17958	Mouse scF
24	935.5	70.7	251	2	AAY17962	Mouse scF
25	935.5	70.7	507	5	AAU72858	8G7C1ox4-
26	935.5	70.7	510	5	AAU72859	6E5A7x4-7
27	935.5	70.7	510	5	AAU72860	Human p53
28	935.5	70.7	532	2	AAY78328	Bispecifi
29	921	69.6	249	2	AAW60770	Single ch
30	914	69.0	543	7	ADD12876	CD28/mela
31	908.5	68.6	291	4	AAB20443	Antibody
32	908.5	68.6	322	4	AAB20440	Antibody
33	908.5	68.6	729	4	AAB20439	Antibody
34	905	68.4	282	2	AAW09818	Antibody
35	905	68.4	282	2	AAW35564	HindIII-E
36	905	68.4	355	2	AAW35133	R. pipien
37	902	68.1	483	3	AAW88099	A protein
38	902	68.1	483	3	AAB07935	A divalen
39	902	68.1	483	3	AAY57254	Divalent
40	902	68.1	483	3	AAB27679	Bivalent
41	902	68.1	483	3	AAY80924	Bivalent
42	902	68.1	483	6	ABU61809	Bivalent
43	902	68.1	486	2	AAR37649	Sequence
44	898.5	67.9	392	3	AAB10863	S11-VEGF2
45	898.5	67.9	510	3	AAB10864	S11-scVEG

ALIGNMENTS

RESULT 1
AAY17964
ID   AAY17964 standard; protein; 248 AA.
XX
AC   AAY17964;
XX
DT   04-AUG-1999 (first entry)
XX
DE   Mouse scFv fragment 5-10.
XX
KW   Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW   autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
OS   Mus sp.
XX
PN   WO9925818-A1.
XX
PD   27-MAY-1999.
XX
PF   16-NOV-1998; 98WO-EP007313.
XX
PR   17-NOV-1997; 97EP-00120096.
XX
PA   (KUFB/) KUFER P.
XX
PI   Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
PT   Phage display system for identification of binding site domains retaining
PT   capacity to bind an epitope.
XX
PS   Claim 27; Fig 6.10; 152pp; English.
XX
CC   The invention relates to a method of identifying binding site domains
CC   (BSD) that retain the capacity of binding to a predetermined epitope when
CC   positioned C-terminal of at least one further domain in a recombinant bi-
CC   or multivalent polypeptide. The method comprises (a) testing a panel of
CC   BSD displayed on the surface of a biological display system as part of a
CC   fusion protein for binding to a predetermined epitope, where the fusion
CC   protein comprises an additional domain positioned N-terminal of the BSD
CC   and an amino acid sequence that mediates anchoring of the fusion protein
CC   to the surface of the display system; and (b) identifying a BSD that
CC   binds to the predetermined epitope. The method is useful to identify bi-
CC   or multivalent polypeptides that comprise antibody binding sites capable
CC   of efficiently binding to the corresponding antigen. The polypeptides or
CC   antibodies identified by the method are useful therapeutically and

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CC  diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC  fragments that bind independently of their position within bifunctional
CC  single-chain fusion proteins can be isolated from combinatorial antibody
CC  libraries using the new in vitro method. Sequences AAY17957-965 represent
CC  mouse scFv fragments
XX
SQ  Sequence 248 AA;

Qy  Query Match     100.0%;  Score 1324;  DB 2;  Length 248;
    Best Local Similarity  100.0%;  Pred. No.2.7e-87;
    Matches 248;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIH   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIH   60

Qy   61  YNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSS  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  YNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSS  120

Qy  121  GGGGSGGGGSGGGGSGGGGSELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQK  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GGGGSGGGGSGGGGSGGGGSELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQK  180

Qy  181  PGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFG  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  PGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFG  240

Qy  241  AGTKLEIK  248
         ||||||||
Db  241  AGTKLEIK  248
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RESULT 2
AAY17960

```
ID   AAY17960 standard; protein; 248 AA.
XX
AC   AAY17960;
XX
DT   04-AUG-1999  (first entry)
XX
DE   Mouse scFv fragment 4-1.
XX
KW   Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW   autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
OS   Mus sp.
XX
PN   WO9925818-A1.
XX
PD   27-MAY-1999.
XX
PF   16-NOV-1998;  98WO-EP007313.
XX
PR   17-NOV-1997;  97EP-00120096.
XX
PA   (KUFE/) KUFER P.
XX
PI   Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR   WPI; 1999-338004/28.
DR   N-PSDB; AAX77243.
XX
PT   Phage display system for identification of binding site domains retaining
PT   capacity to bind an epitope.
XX
PS   Claim 27; Fig 6.6; 152pp; English.
XX
CC   The invention relates to a method of identifying binding site domains
CC   (BSD) that retain the capacity of binding to a predetermined epitope when
CC   positioned C-terminal of at least one further domain in a recombinant bi-
CC   or multivalent polypeptide. The method comprises (a) testing a panel of
CC   BSD displayed on the surface of a biological display system as part of a
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```
CC  fusion protein for binding to a predetermined epitope, where the fusion
CC  protein comprises an additional domain positioned N-terminal of the BSD
CC  and an amino acid sequence that mediates anchoring of the fusion protein
CC  to the surface of the display system; and (b) identifying a BSD that
CC  binds to the predetermined epitope. The method is useful to identify bi-
CC  or multivalent polypeptides that comprise antibody binding sites capable
CC  of efficiently binding to the corresponding antigen. The polypeptides or
CC  antibodies identified by the method are useful therapeutically and
CC  diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC  fragments that bind independently of their position within bifunctional
CC  single-chain fusion proteins can be isolated from combinatorial antibody
CC  libraries using the new in vitro method. Sequences AAY17957-965 represent
CC  mouse scFv fragments
XX
SQ  Sequence 248 AA;

Qy  Query Match     95.2%;  Score 1261;  DB 2;  Length 248;
    Best Local Similarity  95.6%;  Pred. No.9e-83;
    Matches 237;  Conservative  3;  Mismatches  8;  Indels  0;  Gaps  0;

Qy    1  EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIH   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1  EVQLLEQSGAELVRPGTSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNAH   60

Qy   61  YNEKFKGKATLTADKSSSTAYMQLSSLTFEDSAVYFCARLRNWDEPMDYWGQGTTVTVSS  120
         ||||||||||||||||||||||||||||| |||||||||||||||| |||||||||||||
Db   61  YNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARLRNWDEAMDYWGQGTTVTVSS  120

Qy  121  GGGGSGGGGSGGGGSGGGGSELVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQK  180
         |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||| ||||
Db  121  GGGGSGGGGSGGGGSGGGGSELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQK  180

Qy  181  PGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFG  240
         ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  181  PGQPPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPYFG   240

Qy  241  AGTKLEIK  248
         |||||||
Db  241  GGTKLEIK  248
```

RESULT 3
AAY17965

```
ID   AAY17965 standard; protein; 248 AA.
XX
AC   AAY17965;
XX
DT   04-AUG-1999  (first entry)
XX
DE   Mouse scFv fragment 5-13.
XX
KW   Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW   autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
OS   Mus sp.
XX
PN   WO9925818-A1.
XX
PD   27-MAY-1999.
XX
PF   16-NOV-1998;  98WO-EP007313.
XX
PR   17-NOV-1997;  97EP-00120096.
XX
PA   (KUFE/) KUFER P.
XX
PI   Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR   WPI; 1999-338004/28.
DR   N-PSDB; AAX77248.
XX
PT   Phage display system for identification of binding site domains retaining
PT   capacity to bind an epitope.
```